

Title: US-10-088-961-2
 Perfect score: 4395
 Sequence: 1 NSGNNAEEAPGAKAPEPAAA.....KRAERKVAKGPMKLGARKLD 831

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	4395	100.0	832	4	AAB74457	Aab74457 Human Tra
2	4311	98.1	820	3	AAB43354	Aab43354 Human ORF
3	4259	96.9	808	4	AAB65679	Aab65679 Novel pro
4	4148.5	94.4	791	4	AAE11780	Aae11780 Human kin
5	4148.5	94.4	791	5	ABP69655	Abp69655 Human pol
6	3128	71.2	618	4	AAB74769	Aab74769 Human sec
7	3057.5	69.6	675	4	AAM40778	Aam40778 Human pol
8	3054.5	69.5	587	4	AAB74754	Aab74754 Human sec
9	3054.5	69.5	587	5	ABG65328	Abg65328 Human alb
10	2939	66.9	601	7	ADC99070	Adc99070 Human KPP
11	1841	41.9	873	4	ABB58257	Abb58257 Drosophil
12	1839	41.8	524	3	AAB58954	Aab58954 Breast an
13	1750	39.8	410	2	AAW93254	Aaw93254 Human ESR
14	1440	32.8	287	3	AAB35708	Aab35708 Human pro
15	398.5	9.1	688	4	AAB65677	Aab65677 Novel pro
16	396.5	9.0	688	4	AAM39110	Aam39110 Human pol
17	396	9.0	95	4	AAM87919	Aam87919 Human imm
18	376	8.6	694	4	AAM40896	Aam40896 Human pol
19	367.5	8.4	179	3	AAG32991	Aag32991 Arabidops
20	357.5	8.1	929	5	AAE25093	Aae25093 Human kin

21	357.5	8.1	929	7	ADC39226	Adc39226	Novel hum
22	332	7.6	740	4	ABG04490	Abg04490	Novel hum
23	311.5	7.1	835	4	ABB58693	Abb58693	Drosophil
24	290	6.6	796	6	ABO07166	Abo07166	Human p53
25	287.5	6.5	505	4	AAB65678	Aab65678	Novel pro
26	279.5	6.4	641	4	ABB58034	Abb58034	Drosophil
27	267	6.1	792	4	AAB85782	Aab85782	Human kin
28	260	5.9	126	3	AAG32992	Aag32992	Arabidops
29	250	5.7	756	4	AAB95177	Aab95177	Human pro
30	250	5.7	756	4	AAG67427	Aag67427	Amino aci
31	220	5.0	98	3	AAG32993	Aag32993	Arabidops
32	206	4.7	735	4	AAB95772	Aab95772	Human pro
33	206	4.7	735	6	ABO07167	Abo07167	Human p53
34	204	4.6	125	4	AAM96498	Aam96498	Human rep
35	198	4.5	795	5	AAE19052	Aae19052	Human PAR
36	198	4.5	795	5	AAE16258	Aae16258	Human kin
37	198	4.5	795	6	AAE33551	Aae33551	Human mic
38	192	4.4	793	7	ADC34764	Adc34764	Rat serin
39	188.5	4.3	621	4	ABB69056	Abb69056	Drosophil
40	188.5	4.3	786	4	AAU03518	Aau03518	Human pro
41	188	4.3	783	4	AAG65764	Aag65764	Human pro
42	188	4.3	823	3	AAW90879	Aaw90879	Human ker
43	187	4.3	790	3	AAW90878	Aaw90878	Human ker
44	185.5	4.2	782	4	AAM47219	Aam47219	Human NOV
45	185	4.2	779	2	AAR98226	Aar98226	Rat neuro

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 Perfect score: 4395
 Sequence: 1 NSGNNAEEAPGAKAPEPAAA.....KRAERKVAKGPMKLGARKLD 831

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1440	32.8	287	4	US-09-327-983-4	Sequence 4, Appli
2	192	4.4	793	4	US-09-523-849-32	Sequence 32, Appl
3	187	4.3	1317	3	US-09-083-521-7	Sequence 7, Appli
4	184	4.2	779	4	US-08-817-832B-31	Sequence 31, Appl
5	178	4.1	729	2	US-08-677-298-2	Sequence 2, Appli
6	178	4.1	729	4	US-09-523-849-33	Sequence 33, Appl
7	174.5	4.0	1315	3	US-09-031-563-2	Sequence 2, Appli
8	174.5	4.0	1315	3	US-09-031-563-25	Sequence 25, Appl
9	174.5	4.0	1315	4	US-09-293-505-10	Sequence 10, Appl
10	174.5	4.0	1315	4	US-09-392-277-2	Sequence 2, Appli
11	174.5	4.0	1315	4	US-09-392-277-25	Sequence 25, Appl
12	174.5	4.0	1315	4	US-09-258-000-2	Sequence 2, Appli
13	174.5	4.0	1315	4	US-09-258-000-25	Sequence 25, Appl
14	172	3.9	1360	3	US-09-393-569-2	Sequence 2, Appli
15	172	3.9	1360	4	US-09-579-664B-14	Sequence 14, Appl
16	172	3.9	1360	4	US-09-645-456A-34	Sequence 34, Appl
17	172	3.9	1360	4	US-09-425-324A-34	Sequence 34, Appl
18	172	3.9	1360	4	US-09-645-791-34	Sequence 34, Appl
19	169.5	3.9	1306	4	US-09-645-456A-10	Sequence 10, Appl
20	169.5	3.9	1306	4	US-09-425-324A-10	Sequence 10, Appl
21	169.5	3.9	1306	4	US-09-645-791-10	Sequence 10, Appl
22	168.5	3.8	642	4	US-09-371-338-11	Sequence 11, Appl

23	168.5	3.8	1332	4	US-09-645-456A-9	Sequence 9, Appli
24	168.5	3.8	1332	4	US-09-425-324A-9	Sequence 9, Appli
25	168.5	3.8	1332	4	US-09-645-791-9	Sequence 9, Appli
26	167	3.8	722	4	US-09-984-890-4	Sequence 4, Appli
27	166	3.8	1277	4	US-09-645-456A-12	Sequence 12, Appl
28	166	3.8	1277	4	US-09-425-324A-12	Sequence 12, Appl
29	166	3.8	1277	4	US-09-645-791-12	Sequence 12, Appl
30	165.5	3.8	647	3	US-09-031-563-7	Sequence 7, Appli
31	165.5	3.8	647	4	US-09-392-277-7	Sequence 7, Appli
32	165.5	3.8	647	4	US-09-258-000-7	Sequence 7, Appli
33	165.5	3.8	648	3	US-09-031-563-5	Sequence 5, Appli
34	165.5	3.8	648	4	US-09-392-277-5	Sequence 5, Appli
35	165.5	3.8	648	4	US-09-258-000-5	Sequence 5, Appli
36	165	3.8	724	4	US-09-984-890-2	Sequence 2, Appli
37	164	3.7	722	4	US-08-817-832B-32	Sequence 32, Appl
38	163	3.7	1375	3	US-09-171-410-1	Sequence 1, Appli
39	162	3.7	1353	4	US-09-645-456A-11	Sequence 11, Appl
40	162	3.7	1353	4	US-09-425-324A-11	Sequence 11, Appl
41	162	3.7	1353	4	US-09-645-791-11	Sequence 11, Appl
42	160.5	3.7	1601	4	US-09-345-473E-40	Sequence 40, Appl
43	160	3.6	1297	4	US-09-688-188B-14	Sequence 14, Appl
44	160	3.6	1297	4	US-09-291-417D-14	Sequence 14, Appl
45	159.5	3.6	1298	4	US-09-645-456A-14	Sequence 14, Appl

Title: US-10-088-961-2
 Perfect score: 4395
 Sequence: 1 NSGNNAEEAPGAKAPEPAAA.....KRAERKVAKGPMKLGARKLD 831

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	4259	96.9	808	12	US-10-267-502-223	Sequence 223, App
2	4148.5	94.4	791	15	US-10-258-106-14	Sequence 14, Appl
3	3866	88.0	806	12	US-10-267-502-224	Sequence 224, App
4	3128	71.2	618	14	US-10-060-255-78	Sequence 78, Appl
5	3054.5	69.5	587	11	US-09-833-245-2077	Sequence 2077, Ap
6	3054.5	69.5	587	14	US-10-060-255-63	Sequence 63, Appl
7	2087	47.5	435	12	US-10-210-281-44	Sequence 44, Appl
8	1841	41.9	873	12	US-10-267-502-222	Sequence 222, App
9	1839	41.8	524	12	US-09-925-298-662	Sequence 662, App
10	1839	41.8	524	14	US-10-102-806-662	Sequence 662, App

11	548	12.5	482	12	US-10-425-114-37745	Sequence 37745, A
12	515	11.7	452	12	US-10-424-599-230423	Sequence 230423,
13	396.5	9.0	1000	12	US-10-425-114-57734	Sequence 57734, A
14	388.5	8.8	974	12	US-10-425-114-62433	Sequence 62433, A
15	357.5	8.1	929	16	US-10-433-794-13	Sequence 13, Appl
16	277	6.3	175	12	US-10-424-599-178241	Sequence 178241,
17	268.5	6.1	649	12	US-10-424-599-163571	Sequence 163571,
18	256	5.8	307	12	US-10-424-599-231121	Sequence 231121,
19	250	5.7	756	14	US-10-059-585-16	Sequence 16, Appl
20	239.5	5.4	563	12	US-10-425-114-55865	Sequence 55865, A
21	236.5	5.4	176	12	US-10-424-599-273705	Sequence 273705,
22	235.5	5.4	344	12	US-10-425-114-70300	Sequence 70300, A
23	218	5.0	735	12	US-10-425-114-57029	Sequence 57029, A
24	204	4.6	125	10	US-09-764-891-5156	Sequence 5156, Ap
25	202.5	4.6	503	12	US-10-425-114-54113	Sequence 54113, A
26	198	4.5	382	12	US-10-425-114-57771	Sequence 57771, A
27	198	4.5	795	9	US-09-919-585-12	Sequence 12, Appl
28	198	4.5	795	14	US-10-142-356-9	Sequence 9, Appli
29	198	4.5	795	14	US-10-161-565-25	Sequence 25, Appl
30	198	4.5	795	16	US-10-311-034-4	Sequence 4, Appli
31	192	4.4	793	14	US-10-195-101-32	Sequence 32, Appl
32	191	4.3	826	12	US-10-425-114-54182	Sequence 54182, A
33	190.5	4.3	378	12	US-10-424-599-263841	Sequence 263841,
34	190.5	4.3	1246	15	US-10-369-493-6585	Sequence 6585, Ap
35	188.5	4.3	786	10	US-09-823-187-91	Sequence 91, Appl
36	188.5	4.3	786	15	US-10-231-913-118	Sequence 118, App
37	188	4.3	783	9	US-09-815-915-2	Sequence 2, Appli
38	188	4.3	783	14	US-10-393-316-2	Sequence 2, Appli
39	187	4.3	1317	9	US-09-963-896-7	Sequence 7, Appli
40	185.5	4.2	782	10	US-09-823-187-26	Sequence 26, Appl
41	185	4.2	576	12	US-10-425-114-38686	Sequence 38686, A
42	184	4.2	779	8	US-08-817-832B-31	Sequence 31, Appl
43	184	4.2	779	12	US-10-440-435-31	Sequence 31, Appl
44	184	4.2	783	10	US-09-823-187-90	Sequence 90, Appl
45	182.5	4.2	744	9	US-09-919-585-3	Sequence 3, Appli

Title: US-10-088-961-2
 Perfect score: 4395
 Sequence: 1 NSGNNAEEAPGAKAPEPAAA.....KRAERKVAKGPMKLGARKLD 831

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	496	11.3 637	1	YDOD_SCHPO	O13733 schizosacch
2	309.5	7.0 804	1	SCY1_YEAST	P53009 saccharomyc
3	188.5	4.3 786	1	SN1L_HUMAN	P57059 homo sapien
4	176.5	4.0 841	1	NEK4_HUMAN	P51957 homo sapien
5	172.5	3.9 752	1	MRK4_HUMAN	Q96134 homo sapien
6	172	3.9 1360	1	TNIK_HUMAN	Q9uke5 homo sapien
7	164	3.7 714	1	HUNK_HUMAN	P57058 homo sapien
8	164	3.7 794	1	KI11_HUMAN	Q8tdc3 homo sapien
9	160.5	3.7 1374	1	M3K5_HUMAN	Q99683 homo sapien
10	160	3.6 1258	1	NEK1_HUMAN	Q96py6 homo sapien
11	159.5	3.6 776	1	MRK3_HUMAN	P27448 homo sapien
12	158	3.6 1379	1	M3K5_MOUSE	O35099 mus musculu
13	157.5	3.6 774	1	NEK1_MOUSE	P51954 mus musculu
14	154	3.5 714	1	HUNK_MOUSE	O88866 mus musculu
15	154	3.5 888	1	M3KC_RAT	Q63796 rattus norv
16	152	3.5 1505	1	CUT1_HUMAN	P39880 homo sapien
17	150	3.4 1039	1	GUNB_CALSA	P10474 c endogluca
18	148	3.4 1442	1	DAK1_MOUSE	Q80ye7 mus musculu
19	147.5	3.4 1331	1	MANB_CALSA	P22533 caldocellum
20	147.5	3.4 1895	1	WR19_ARATH	Q9sz67 arabidopsis
21	147	3.3 683	1	PLO1_SCHPO	P50528 schizosacch
22	147	3.3 888	1	M3KC_MOUSE	Q60700 mus musculu
23	146	3.3 1217	1	AF4_MOUSE	O88573 mus musculu
24	145	3.3 603	1	PLK1_HUMAN	P53350 homo sapien
25	144.5	3.3 2142	1	BAT2_HUMAN	P48634 homo sapien
26	144	3.3 646	1	CNK_HUMAN	Q9h4b4 homo sapien
27	144	3.3 779	1	SN1L_MOUSE	Q60670 mus musculu
28	144	3.3 1308	1	M4K6_MOUSE	Q9jm52 mus musculu

29	143.5	3.3	774	1	MRK2_MOUSE	Q05512	mus	musculu
30	143.5	3.3	1395	1	CUT1_MOUSE	P53564	mus	musculu
31	143.5	3.3	1863	1	BRC1_HUMAN	P38398	homo	sapien
32	143	3.3	984	1	NEK9_MOUSE	Q8k1r7	mus	musculu
33	142.5	3.2	511	1	NEK3_MOUSE	Q9r0a5	mus	musculu
34	142	3.2	776	1	SN1L_RAT	Q9rlu5	rattus	norv
35	142	3.2	1742	1	GUNA_CALSA	P22534	caldocellu	
36	141.5	3.2	576	1	POLO_DROME	P52304	drosophila	
37	141.5	3.2	736	1	ST29_HUMAN	Q8iwq3	homo	sapien
38	141	3.2	685	1	SNK_HUMAN	Q9nyy3	homo	sapien
39	140.5	3.2	1123	1	ABL1_MOUSE	P00520	mus	musculu
40	140	3.2	792	1	NEK4_MOUSE	Q9z1j2	mus	musculu
41	139	3.2	431	1	NRKA_TRYBB	Q08942	trypanosoma	
42	139	3.2	859	1	M3KC_HUMAN	Q12852	homo	sapien
43	139	3.2	1030	1	STK9_HUMAN	O76039	homo	sapien
44	138.5	3.2	305	1	PH85_YEAST	P17157	saccharomyc	
45	138	3.1	682	1	SNK_MOUSE	P53351	mus	musculu

Title: US-10-088-961-2
 Perfect score: 4395
 Sequence: 1 NSGNNAEEAPGAKAPEPAAA.....KRAERKVAKGPMKLGARKLD 831

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	1214	27.6	820	2	T26272
2	875.5	19.9	604	2	B84833
3	496	11.3	637	2	T37713
4	393	8.9	761	2	S60992
5	354.5	8.1	749	2	T50397
6	309.5	7.0	804	2	S64090
7	308	7.0	759	2	F86362
8	207.5	4.7	1192	2	T18611
9	202	4.6	689	2	T29772
10	190.5	4.3	1246	2	G89287
11	187	4.3	1317	2	T03748
12	176.5	4.0	841	1	I78885
13	171.5	3.9	372	2	T52621
14	169.5	3.9	651	2	A96591
15	166.5	3.8	713	2	S27966
16	161.5	3.7	1870	2	S37671
17	161.5	3.7	1872	2	S36152
18	160.5	3.7	745	2	G01025
19	160.5	3.7	1851	2	T19964
20	159	3.6	888	2	JC5399
21	158	3.6	887	2	T20941
22	158	3.6	1379	2	JC5778
23	157.5	3.6	774	2	S25284
24	157.5	3.6	1398	2	T13741

25	156.5	3.6	421	2	T48202	protein kinase AK2
26	150	3.4	1039	2	S02711	cellulase (EC 3.2.
27	148.5	3.4	1231	2	T18532	serine/threonine pr
28	147.5	3.4	1211	2	T42230	AF4 protein - mous
29	147.5	3.4	1331	2	A48954	mannan endo-1,4-be
30	147.5	3.4	1423	1	I37275	death-associated p
31	147.5	3.4	1895	2	T06609	disease resistance
32	147	3.3	480	2	A86371	hypothetical prote
33	147	3.3	683	2	T38254	serine/threonine-s
34	147	3.3	888	2	A55318	serine/threonine p
35	146	3.3	1217	2	T42625	AF-4 protein - mou
36	145.5	3.3	3429	2	T13853	hypothetical prote
37	145	3.3	479	2	T46318	hypothetical prote
38	145	3.3	603	2	S34130	serine/threonine-s
39	144.5	3.3	476	2	T47807	hypothetical prote
40	144.5	3.3	1233	2	T14157	serine/threonine p
41	144.5	3.3	2142	2	B35098	MHC class III hist
42	143.5	3.3	608	2	T01833	serine/threonine-s
43	143.5	3.3	774	2	I48609	probable serine/th
44	143.5	3.3	836	2	B96716	probable serine/th
45	143.5	3.3	1206	2	T34021	protein kinase SK2

Title: US-10-088-961-2
 Perfect score: 4395
 Sequence: 1 NSGNNAEEAPGAKAPEPAAA.....KRAERKVAKGPMKLGARKLD 831

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL_25:*
 1: sp_archaea:*
 2: sp_bacteria:*
 3: sp_fungi:*
 4: sp_human:*
 5: sp_invertebrate:*
 6: sp_mammal:*
 7: sp_mhc:*
 8: sp_organelle:*
 9: sp_phage:*
 10: sp_plant:*
 11: sp_rodent:*
 12: sp_virus:*
 13: sp_vertebrate:*
 14: sp_unclassified:*
 15: sp_rvirus:*
 16: sp_bacteriap:*
 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query			Description
	No.	Score	Match	Length	ID	
1	4259	96.9	808	4	Q96KG9	Q96kg9 homo sapien
2	4148.5	94.4	791	4	Q96KG8	Q96kg8 homo sapien
3	3866	88.0	806	11	Q8K222	Q8k222 mus musculu
4	3865	87.9	806	11	Q9EQC5	Q9eqc5 mus musculu
5	3639.5	82.8	707	4	Q96KH1	Q96kh1 homo sapien
6	3345	76.1	786	4	Q9HAW5	Q9haw5 homo sapien
7	2063	46.9	425	4	Q96G50	Q96g50 homo sapien
8	1841	41.9	873	5	Q9VAH7	Q9vah7 drosophila
9	1526	34.7	283	4	Q9NR53	Q9nr53 homo sapien
10	1263.5	28.7	270	4	Q9HBL3	Q9hbl3 homo sapien
11	1214	27.6	820	5	Q23215	Q23215 caenorhabdi

12	1039	23.6	800	10	Q8LQE7	Q8lqe7 oryza sativ
13	917	20.9	776	3	Q9HEA4	Q9hea4 neurospora
14	875.5	19.9	604	10	Q7XJN7	Q7xjn7 arabidopsis
15	410	9.3	735	11	Q9DBQ7	Q9dbq7 mus musculu
16	409.5	9.3	742	4	Q8IZE3	Q8ize3 homo sapien
17	401.5	9.1	768	13	Q803U0	Q803u0 brachydanio
18	398.5	9.1	688	4	Q9UBK6	Q9ubk6 homo sapien
19	397.5	9.0	688	4	Q8IZN9	Q8izn9 homo sapien
20	396.5	9.0	688	4	Q96C56	Q96c56 homo sapien
21	393	8.9	761	3	Q12453	Q12453 saccharomyc
22	384.5	8.7	850	5	Q8I466	Q8i466 plasmodium
23	358.5	8.2	930	11	Q8CFE4	Q8cfe4 mus musculu
24	354.5	8.1	749	3	Q9P7X5	Q9p7x5 schizosacch
25	331	7.5	909	10	Q9C9H8	Q9c9h8 arabidopsis
26	311.5	7.1	835	5	Q9VAR0	Q9var0 drosophila
27	309.5	7.0	963	10	Q9ASH9	Q9ash9 oryza sativ
28	308	7.0	759	10	O23135	O23135 arabidopsis
29	290	6.6	796	4	Q9P2I7	Q9p2i7 homo sapien
30	279.5	6.4	641	5	Q9Y0Z6	Q9y0z6 drosophila
31	271	6.2	799	3	Q874M0	Q874m0 kluyveromyc
32	250	5.7	756	4	Q96ST4	Q96st4 homo sapien
33	234	5.3	789	5	O01776	O01776 caenorhabdi
34	209.5	4.8	1096	5	Q17368	Q17368 caenorhabdi
35	207.5	4.7	1192	5	Q9TW45	Q9tw45 caenorhabdi
36	207.5	4.7	1192	5	Q17346	Q17346 caenorhabdi
37	207	4.7	507	11	Q8BRJ1	Q8brj1 mus musculu
38	206	4.7	735	4	Q9H7V5	Q9h7v5 homo sapien
39	198	4.5	795	4	Q9P0L2	Q9p0l2 homo sapien
40	196.5	4.5	776	13	Q7ZYL7	Q7zyl7 xenopus lae
41	196.5	4.5	785	13	Q8QGV3	Q8qgv3 xenopus lae
42	192	4.4	793	11	O08678	O08678 rattus norv
43	191.5	4.4	1066	5	Q8MVX0	Q8mvx0 haemonchus
44	189	4.3	795	11	Q8VHJ5	Q8vhj5 mus musculu
45	188.5	4.3	621	5	Q9VT71	Q9vt71 drosophila